



Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro  
 65 70 75 80  
  
 tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag 288  
 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln  
 85 90 95  
  
 ttc tcc ctg aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat 336  
 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr  
 100 105 110  
  
 tac tgt gcg aga gaa ata gca gct cgt cct cac cga tac ttt gac tac 384  
 Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr  
 115 120 125  
  
 tgg ggc cag gga acc ctg gtc acc gtc tcc tca 417  
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 130 135  
  
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 <213> Homo sapiens  
  
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 Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys  
 20 25 30  
  
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe  
 35 40 45  
  
 Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu  
 50 55 60  
  
 Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro  
 65 70 75 80  
  
 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln  
 85 90 95  
  
 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr  
 100 105 110  
  
 Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr

115

120

125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
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&lt;210&gt; 3

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(351)

&lt;220&gt;

&lt;221&gt; sig\_peptide

&lt;222&gt; (1)..(24)

&lt;400&gt; 3

ctc tgg ctc cca gat acc act gga gaa ata gtg atg acg cag tct cca 48  
 Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val Met Thr Gln Ser Pro  
 1 5 10 15

gcc acc ctg tct gtg tct cca ggg gaa aga gcc acc ctc tcc tgc agg 96  
 Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg  
 20 25 30

gcc agt cag agt gtt agc agc aac tta gcc tgg tac cag cag aaa cct 144  
 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro  
 35 40 45

ggc cag gct ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act 192  
 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr  
 50 55 60

ggt atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gag ttc act 240  
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr  
 65 70 75 80

ctc acc atc agc agc ctg cag tct gaa gat ttt gca gtt tat tac tgt 288  
 Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys  
 85 90 95

cag cag tat aat aac tgg cct ccg tac act ttt ggc cag ggg acc aag 336  
 Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys  
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ctg gag atc aaa cga  
 Leu Glu Ile Lys Arg  
 115

351

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 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro  
 35 40 45  
 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr  
 50 55 60  
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr  
 65 70 75 80  
 Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys  
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 Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys  
 100 105 110  
 Leu Glu Ile Lys Arg  
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<210> 5  
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 <212> DNA  
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<220>  
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<400> 5  
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 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser





